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16
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                HSM807863
                                                      AF518122
AF518122
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HS46A3F
                                                                                                                                                                                                             IJ
     AX345003
                                    BC068189
                                                                                     BV070170
IMA295790
                                                                                                                                                                     CQ709049
                                                                                                                                                  G81093
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                                                                                         Z55508 H. sapiens C
Z55508 H. sapiens C
CQ709049 Sequence
CQ709049 Sequence
G81093 S208P6414RC
G81093 S208P6414RC
AB165691 Bos tauru
AB165691 Bos tauru
AB165691 Bos tauru
BV070170 S208P6211
BV070170 S208P6211
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Templeton
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Danio rer
              Homo sapi
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Isolepis
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AUTHORS
TITLE
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VERSION
KEYWORDS
                                 ORIGIN
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TITLE
Query Match
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                                                                                                                                                                                                                                                              MEDLINE
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/clone_lib="CGI-1"
/dev_stage="adult"
                                                                        sex="male"
                                                                                 lone="46a3"
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 100.0%;
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| | 28833 | 26246 | 26246 | 23579 | 23579 | 23501 | 23501 | 8617 | 8617 | 7823 | 7823 | 7823 | 7823 | 7823 | 7823 | 7823 | 7823 | 7733 | 7733 | 6992 | 6992 | 6059 | 6059 | 6059 | 6059 | .5728 |
| | 9 | w | w | σ | σ | 9 | 9 | w | w | σ | 6 | σ | σ | 6 | თ | σ | σ | ω | ω | Φ | σ | 9 | 9 | 9 | 9 | σ |
| | AC096581 | CET12G3 | CET12G3 | AX647373 | AX647373 | AC126176 | AC126176 | DMU19731 | DMU19731 | AX346962 | AX346962 | AX344488 | AX344488 | AX323803 | AX323803 | AX278034 | AX278034 | DROAGPDHD | DROAGPDHD | CQ593660 | CQ593660 | AY037299 | AY037299 | AB023158 | AB023158 | AX345003 |
| • | œ | | Ō. | AX647373 Sequence | | | | | ĸ | | | Sequenc | | AX323803 Sequence | | AX278034 Sequence | w | | D50090 Drosophila | | Seque | 9 Homo | Homo | 8 Homo | AB023158 Homo sapi | AX345003 Sequence |

ALIGNMENTS

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2 (bases 1 to 103)

MacDonald,M., Huckle,E., Wilkinson,P. and Micklem,G.

Direct Submission

Submitted (16-0CT-1995) The Sanger Centre, Hinxton, Cambridgeshire,

CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk

Vector: pGEM-5Zf(-)
                                                                                                      or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                           Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.mrc.ac.uk/ for details
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P. Purification of CpG islands using a methylated Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1e 46a3, forward
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Length 103;

Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Database
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Maximum DB seq length: 2000000000
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16
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geneseqn1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| AAK78540 AAK78540 | AAK78539 | AAK77535 | AAK77535 | ABN87608 | ABN87608 | AAD44422 | AAD44422 | ABN87612 | ABN87612 | ABN87618 | ABN87618 | ABN87619 | ABN87619 | ABN87617 | ABN87617 | ABN87616 | ABN87616 | ID |
| | Aak78539] Aak78539] | | | | | | | | | | | _ | Φ | 7 | _ | Abn87616 | Abn87616 | Description |
| Human imm Human imm | Human imm Human imm | | Human imm | Arabidops | Arabidops | PCR prime | PCR prime | Arabidops | Arabidops | Native in | on . |

| 45 | C 44 | 43 | C 42 | 41 | c 40 | 39 | c 38 | . 37 | c 36 | 35 | c 34 | 33 | c 32 | 31 | c 30 | 29 | c 28 | 27 | c 26 | 25 | c 24 | 23 | c 22 | 21 |
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| ABD32911_6 | DQ59398_2 | DQ59398 2 | ABS55320_2 | ABS55320_2 | ABS55320 4 | ABS55320_4 | ADQ09371 | ADQ09371 | ACN44860 | ACN44860 | ADC87112 | ADC87112 | ABK28417 | ABK28417 | ABK31492 | ABK31492 | ABL34060 | ABL34060 | AAS45489 | AAS45489 | ABL16118 | ABL16118 . | ABL32101 | ABL32101 |
| Cor | Co | Col | Cont | Cont | Cont | Cont | Ado | Ado | Acı | Acı | Adı | Adı | Abk | Abk | Abk | Abk | Ab1: | Ab1: | Aas | Aas | Ab1 | Ab1 | Ab1 | Ab1 |
| Continuation (7 of | ω | Continuation (3 of | <u>3</u> | Continuation (3 of | | Continuation (5 of | Human | Human | Acn44860 Mouse gen | Acn44860 Mouse gen | Adc87112 Human GPC | Adc87112 Human GPC | Abk28417 DNA trans | Abk28417 DNA trans | Abk31492 Signal tr | bk31492 Signal tr | 1bl34060 Human imm | bl34060 Human imm | Aas45489 Chemicall | Aas45489 Chemicall | Abl16118 Drosophil | Abl16118 Drosophil | Abl32101 Human imm | Abl32101 Human imm |

ALIGNMENTS

ABN87616; ABN87616 standard; DNA; 16 BP.

Native insulator probe NI16 SEQ ID NO:9.

07-AUG-2002 (first entry)

transgenic plant; probe; Arabidopsis thaliana; genetic insulator; gene promoter; plant; 88.

Arabidopsis thaliana.

WO200234035-A1.

02-MAY-2002.

11-OCT-2001; 2001WO-US031712.

20-OCT-2000; 2000US-0241735P.

(KENT.) UNIV KENTUCKY RES FOUND

Gan S, Xie M;

WPI; 2002-471421/50.

New isolated or recombinant polynucleotide cloned from Arabidopsis thaliana, useful for minimizing or eliminating the position effect transgene in a plant. 9 g

Claim 1; Page 21; 45pp; English.

RESULT 1
ABN87616
ID ABN8
XX
ABN8
XX
ADD O7-A
XX
DE Nati
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AFAB
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PN WO20
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I 1-0
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I 1-0
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I CEN
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I CEN
XX
I CHAI
XX
I The present invention describes an isolated or a recombinant polynucleotide (I) comprising at least one copy of a polynucleotide having the sequence GARTATMATATAT (S1) of 16 nucleotides, or a polynucleotide which is a variant or fragment of S1, where the variant or fragment has a plant genetic insulator activity. Also described are methods: (1) (M1) expressing a polypeptide in a plant cell, involving providing a vector comprising (I), a structural polynucleotide coding for a polypeptide, inserting the vector into a plant cell, where the genetic

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Result
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'Cgm2 6/ptodata/2/pubpna/US09 NEW PUB.seq: 
'Cgm2 6/ptodata/2/pubpna/US10B PUBCOMB.seq: 
'Cgm2 6/ptodata/2/pubpna/US10F PUBCOMB.seq: 
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_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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| equence 1909, | equence 291, | equence 291, i | e 2033, | e 203 | e 197, | | 74, | 74, | Φ | | • | equence 14501 | equence 14501 | equence 14501 | 145 | Sequence 145013, | e 319 | Φ. | e 31928 | e 31928 | e 27290 | Sequence 272906, | e 27290 | 27290 | e 25880, | 25880, | e 53975, | Sequence 53975, A | 53975, | 53975, | Sequence 72551, A | ce 72 | equence 1, | equence 1, | equence 5 | Ф 5 | equence 12, |

ALIGNMENTS

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LENGTH: 16;
TYPE: DIA;
ORGANISM: Arabidopsis thaliana
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICANT: University of Kentucky Research Foundation
APPLICANT: GEN, Susheng
APPLICANT: XIE, Mindtang
TITLE OP INVENTION: Genetic Insulator for Preventing Influence By Another Gene
FILE REFERENCE: 050229-0287
CURRENT APPLICATION NUMBER: US/09/973,945A
CURRENT FILING DATE: 2001-10-11
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,735
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
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                                                                      Conservative
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| 430 | 428 | 428 | 398 | 398 | 393 | 393 | 379 | 379 | 374 | 374 | 365 | 365. | 352 | 352 | 352 | 352 | 338 | 338 | 330 | 330 |
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL RESULT 1 BQ173432 LOCUS FEATURES SOURCE ORGANISM ACCESSION VERSION COMMENT DEFINITION KEYWORDS source Seq primer: 1/ High quality sequence stop: 113. Location/Qualifiers Contact: Maizels RM Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, West Mains Road, Edinburgh EH93JT, Scotland Plate: 03 row: Seg primer: T7 Prof. R. Maizels. Sequencing was sequence contained a PolyA tail (PCR PRimers Echinococcus granulosus Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda; sequence BQ173432 BQ173432.2 GI:23188133 BQ173432 113 pp mknn 111, pp the manne 11, pp mknn 11, pp mknn 12, pp psgr 03G05 T7 Echinococcus granulosus protoscolex (full length enriched) Echinococcus granulosus cDNA clone Eg_PSGR_03G05 5', mRNA On Apr 29, 2002 this sequence version replaced gi:20337834. A survey of genes expressed in Echinococus granulosus metacestode Unpublished (2001) 1 (bases 1 to 113) Fernandez, C. and Maizels, R.M. Tel: +44 131 650 5511 Fax: +44 131 650 5450 Echinococcus granulosus BACKWARD: M13R FORWARD: M13F Yclophyllidea; Taeniidae; Echinococcus. il: T.maizels@ed.ac.uk library was created by Dr Cecilia Fernandez in conjunction with /note="Vector: pSPORT1; Site_1: Sall (5'end); Site_2: NotI (3'end); Echinococcus granulosus is a cestode parasite of dogs (definitive host) and various domestic and wild animals as well as humans (intermediate hosts). The /mol_type="mRNA" /db_xref="taxon:6210" /db_xref="taxon:6210" /clone="kg-R03605" /clone="kg-larva (protoscolex)" /clone_lb="Echinococcus granulosus protoscolex (full length_enriched)" organism="Echinococcus row: G column: 05 granulosus"

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Length 48;

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| US-09-545-244A-8/c US-09-545-244A-8/c ; Sequence 8, Application US/09545244A ; Patent No. 6388170 ; GENERAL INFORMATION: ; APPLICANT: Gan, Susheng ; APPLICANT: Xie, Mingtang ; APPLICANT: Xie, Mingtang ; APPLICANT: No. Bidirectional Promoters and Methods Related Thereto ; TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto ; TUTLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto | Query Match 100.0%; Score 16; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0 Qy 1 GAATATATATATTATTC 16 | RESULT 1 US-09-545-244A-8 Sequence 8, Application US/09545244A Sequence 8, Application US/09545244A Retent No. 63BB270; GENERAL IMPERIATION: APPLICANT: Gan, Susheing APPLICANT: He, Yuehui TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto FILE REFERENCE: 050229-0210; CURRENT APPLICATION NUMBER: US/09/545,244A; CURRENT FILING DATE: 2000-04-07; NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1 SEQ ID NO 8 LENGTH: 48 TYPE: DNA ORGANISM: synthetic construct US-09-545-244A-8 | C 28 15 93.8 488 4 US-09-270-767-5493 29 15 93.8 488 4 US-09-270-767-20775 C 30 15 93.8 488 4 US-09-270-767-20775 C 31 15 93.8 570 4 US-09-949-016-130195 C 32 15 93.8 600 4 US-09-949-016-130195 C 34 15 93.8 600 4 US-09-270-767-10320 C 34 15 93.8 601 4 US-09-270-767-10320 C 36 15 93.8 601 4 US-09-949-016-135263 C 38 15 93.8 601 4 US-09-949-016-135263 C 38 15 93.8 601 4 US-09-949-016-135263 C 38 15 93.8 601 4 US-09-949-016-135263 C 39 15 93.8 601 4 US-09-949-016-135263 C 40 15 93.8 601 4 US-09-949-016-153591 C 40 15 93.8 601 4 US-09-949-016-153591 C 42 15 93.8 601 4 US-09-949-016-153591 C 44 15 93.8 601 4 US-09-949-016-153592 C 42 15 93.8 601 4 US-09-949-016-153592 C 43 15 93.8 601 4 US-09-949-016-153592 C 44 15 93.8 836 4 US-09-949-016-153592 C 44 15 93.8 836 4 US-09-270-767-28507 C 44 15 93.8 836 4 US-09-270-767-28507 Sequence 28507, Ap ALIGNMENTS ALIGNMENTS |
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